

Additional file 4 Putative secretory pathway proteins

Contig	Predicted function ^a	ID	Organism	E value	BIT scores	Identities
Secretion-related ER chaperones, foldases						
Asp84	BIPA - protein translocation, folding, quality control	Y08868	<i>Aspergillus niger</i>	1e-70	268	138/157 (87%)
Asp177	kexin - release of mature proteins from their proproteins by cleavage	CAB64692	<i>Aspergillus niger</i>	2e-78	295	148/183 (80%)
Asp494	Homologous to protein kinase - Component of the unfolded protein response pathway (UPR)	AAP92915	<i>Hypocrea jecorina</i>	2e-43	178	100/181 (55%)
Asp662	cyclophilin-like peptidyl prolyl cis-trans isomerase (cypB) - folding of proteins	AY005867	<i>Aspergillus niger</i>	4e-66	251	125/138 (90%)
Asp734	Protein disulfide-isomerase A (PDIA)	X98797	<i>Aspergillus niger</i>	e-109	399	195/195 (100%)
Asp1020	tigA - disulfide bond formation and isomerization, folding of proteins	X98748	<i>Aspergillus niger</i>	0.0	671	336/356 (94%)
Asp1559	KAR2-homolog of the mammalian BiP/GRP78 gene-protein folding and translocation	AAA34714	<i>Saccharomyces cerevisiae</i>	2e-88	330	169/262 (64%)
Asp1882	calnexin - folding and control of glycoproteins	CAC82717	<i>Aspergillus niger</i>	0.0	903	446/514 (86%)
Asp1902	Protein disulfide-isomerase A (PDIA)	X98797	<i>Aspergillus niger</i>	e-130	467	234/248 (94%)
Asp2143	HSP70- protein folding	AY360059	<i>Trichophyton verrucosum</i>	0.0	993	511/610 (83%)
Asp2274	Homologous to peptidyl-prolyl cis-trans isomerase; fk506-binding protein	NP_595257	<i>Schizosaccharomyces pombe</i>	6e-22	105	48/63 (76%)
Asp2680	Weakly similar to fk506-binding protein 2 precursor (peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (FKBP-21) (NcFKBP22)	O60046	<i>Neurospora crassa</i>	1e-15	86.3	39/53 (73%)
Asp4188	PDI related protein A (prpA)- disulfide bond formation and isomerization, folding of proteins	AF095899	<i>Aspergillus niger</i>	e-110	400	201/208 (96%)
Asp4603	Homologous to proteasome regulatory subunit 12 - eliminating missfolding proteins	AAB84057	<i>Hypocrea jecorina</i>	2e-48	196	96/132 (72%)
Asp5123	Similar to cyclophilin-type peptidyl-prolyl cis-trans isomerase protein	NP_587769	<i>Schizosaccharomyces pombe</i>	2e-31	140	71/152 (46%)

Genes involved in protein transport, protein targeting and vesicle-mediated transport						
Asp70	secretion related GTPase (SrgB) , YptA- ER-Golgi transport YPT1_YEAST GTP-binding protein YPT1 (Protein YP2)	CAC17833 AAF63333 P01123	<i>Aspergillus niger</i> <i>Aspergillus niger</i> <i>var. awamori</i> <i>Saccharomyces cerevisiae</i>	2e-78 4e-78 8e-65	294 293 249	145/145 (100%) 144/145 (99%) 120/147 (81%)
Asp117	Vacuolar protein sorting 16 (hVPS16)	Q9H269	<i>Homo sapiens</i>	8e-34	149	84/186 (45%)
Asp154	Similar to gcs1/glo3/sps18 family zinc finger protein; arfgap gtp-ase activating protein	NP_594843	<i>Schizosaccharomyces pombe</i>	1e-41	174	130/393 (33%)
Asp158	Similar to protein that localized to COPII-coated vesicles, involved in vesicle formation and incorporation of specific secretory cargo	NP_011461	<i>Saccharomyces cerevisiae</i>	3e-41	169	79/131 (60%)
Asp171	probable clathrin assembly protein AP47	CAD70726	<i>Neurospora crassa</i>	3e-49	199	100/116 (86%)
Asp214	Similar to exocyst complex 70 kda component	CAE85518	<i>Neurospora crassa</i>	9e-40	168	100/257 (38%)
Asp276	signal recognition particle (SRP) 54 kd protein homolog	Q00179	<i>Aspergillus niger</i>	e-103	379	196/197 (99%)
Asp290	Similar to coatomer beta subunit	NP_595403	<i>Schizosaccharomyces pombe</i>	5e-53	213	117/195 (60%)
Asp341	YP51_YEAST GTP-binding protein YPT51/VPS21	P36017	<i>Saccharomyces cerevisiae</i>	3e-49	197	96/125 (76%)
Asp383	Homologous to coatomer gamma-2 subunit	CAE76361	<i>Neurospora crassa</i>	e-130	468	242/305 (79%)
Asp444	syntaxin homologue [aspergillus oryzae] similar to S. cerevisiae SED5"	BAC79150	<i>Aspergillus oryzae</i>	9e-58	227	122/136 (89%)
Asp457	Similar to kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 2 [Mus musculus]	NP_080117	<i>Mus musculus</i>	1e-66	255	127/212 (59%)
Asp550	Similar to t-snare of the plasma membrane; sec9p	NP_011523	<i>Saccharomyces cerevisiae</i>	6e-18	96.3	49/108 (45%)
Asp581	NsfA - putative vesicular transport and membrane fusion protein; sec18 homolog	AAF63332	<i>Aspergillus niger</i>	e-125	451	232/232 (100%)
Asp586	Homologous to endoplasmic reticulum calcium transporter	CAE11789	<i>Ustilago maydis</i>	e-116	423	215/333 (64%)
Asp635	Weakly similar to v-snare binding protein; uba domain; n terminal exon may be incorrect	NP_593222	<i>Schizosaccharomyces pombe</i>	1e-11	72.4	46/146 (31%)
Asp641	Similar to coatomer gamma-2 subunit	CAE76361	<i>Neurospora crassa</i>	6e-30	136	69/99 (69%)
Asp757	Similar to vesicle transport v-snare protein	NP_596668	<i>Schizosaccharomyces pombe</i>	4e-23	110	64/154 (41%)
Asp915	Homologous to coatomer alpha subunit	AAC18088	<i>Aspergillus nidulans</i>	e-143	512	269/359 (74%)
Asp953	hypothetical protein AN1768.2 - intra-Golgi transport, secretion related	EAA63944	<i>Aspergillus nidulans</i>	5e-21	106	54/58 (93%)

Asp1003	Homologous to adapter-related protein complex 1 beta 1 subunit (beta-adaptin 1) (Adaptor protein complex AP-1 beta-1 subunit) (Golgi adaptor HA1/AP1 adaptin beta subunit) (Clathrin assembly protein complex 1 beta large chain)	O35643	<i>Mus musculus</i>	e-104	382	190/316 (60%)
Asp1139	Homologous to Gdi1p - regulates vesicle traffic in secretory pathway by regulating dissociation of GDP from Sec4/Ypt/rab family of GTP-binding proteins	NP_011062	<i>Saccharomyces cerevisiae</i>	7e-64	248	165/223 (73%)
Asp1217	small GTPase AvaA, containing Rab subfamily of small GTPases domain	BAB88682	<i>Aspergillus nidulans</i>	e-107	389	194/205 (94%),
Asp1218	Similar to coatmer protein complex subunit beta 2	NP_001001940	<i>Danio rerio</i>	e-103	380	187/368 (50%)
Asp1274	vpsa - involved in vacuolar protein sorting	BAB78398	<i>Aspergillus nidulans</i>	0.0	830	422/462 (91%)
Asp1296	Similar to translocation protein sec62	Q99161	<i>Yarrowia lipolytica</i>	2e-10	70.1	38/88 (43%)
Asp1361	putative vacuolar protein; beta-catenin family	NP_595238	<i>Schizosaccharomyces pombe</i>	2e-62	243	123/168 (73%)
Asp1389	Similar to Gdi1p - Regulates vesicle traffic in secretory pathway by regulating dissociation of GDP from Sec4/Ypt/rab family of GTP-binding proteins	NP_011062	<i>Saccharomyces cerevisiae</i>	5e-59	231	115/193 (59%)
Asp1390	Similar to rer1 homolog - Golgi proteins involved in ER retention(RER)	NP_080671	<i>Mus musculus</i>	1e-33	145	70/115 (60%)
Asp1452	Defective in vacuolar protein sorting; homologous to mouse SKD1 and to human hVPS4; Vps4p	NP_015499	<i>Saccharomyces cerevisiae</i>	4e-41	172	97/233 (41%)
Asp1484	Similar to Pmr1p - involved in Ca2+ dependent processes such as protein sorting, processing, and degradation in the Golgi	NP_011348	<i>Saccharomyces cerevisiae</i>	1e-56	225	140/366 (38%)
Asp1597	Similar to ACR190Cp - Golgi to plasma membrane transport, exocytosis	NP_983592	<i>Eremothecium gossypii</i>	1e-56	225	128/391 (32%)
Asp1610	YP31_YEAST GTP-binding protein YPT31/YPT8	P38555	<i>Saccharomyces cerevisiae</i>	1e-69	265	127/179 (70%)
Asp1619	Weakly similar to snare protein; nsyn1 encode syntaxin homologs (post-Golgi t-SNAREs);	AAF72704	<i>Neurospora crassa</i>	4e-33	145	89/289 (30%)
Asp1630	Homologous to coatmer delta subunit	NP_588336	<i>Schizosaccharomyces pombe</i>	6e-55	216	117/197 (59%)
Asp1708	YP52_YEAST GTP-binding protein YPT52	P36018	<i>Saccharomyces cerevisiae</i>	6e-36	153	91/190 (47%)
Asp1774	Homologous to synaptobrevin-like v snare protein	NP_596561	<i>Schizosaccharomyces</i>	5e-28	126	61/98 (62%)

	[schizosaccharomyces pombe]		<i>pombe</i>			
Asp1811	arf_ajeca adp-ribosylation factor, fgsc a4 - may modulate vesicle budding and uncoating within the Golgi apparatus	EAA66244	<i>Aspergillus nidulans</i>	2e-99	363	179/183 (97%)
Asp1824	RAS protein, containing Rab subfamily of small GTPases domain	CAC17832	<i>Aspergillus niger</i>	2e-27	124	71/201 (35%)
Asp1866	Weakly similar to Nce102p - involved in secretion of proteins that lack classical secretory signal sequences	NP_015475	<i>Saccharomyces cerevisiae</i>	2e-13	77.8	53/143 (37%)
Asp1874	Homologous to cytoplasmic protein involved in release of transport vesicles from the ER; Sec13p	NP_013309	<i>Saccharomyces cerevisiae</i>	2e-75	285	144/240 (60%)
Asp1880	Putative sec61	AAQ72809	<i>Aspergillus awamori</i>	e-148	528	269/269 (100%)
Asp2016	Cdc48p- microsomal protein of CDC48 family of ATPases; involved in secretion, peroxisome formation and gene expression	AAM08677	<i>Aspergillus fumigatus</i>	0.0	1466	750/820 (91%)
Asp2214	Similar to protein that forms a heterotrimeric complex with erp1, erp2p, and Emp24, member of the p24 family involved in endoplasmic reticulum to Golgi transport; Erv25p	NP_013701	<i>Saccharomyces cerevisiae</i>	5e-49	196	95/193 (49%)
Asp2357	Weakly similar to golgi-localized protein with homology to gamma-adaptin, interacts with and regulates Arf1p and Arf2p in a GTP-dependent manner in order to facilitate traffic through the late Golgi; Gga2p	NP_011976	<i>Saccharomyces cerevisiae</i>	9e-17	92.0	62/183 (33%)
Asp2417	ACR190Cp - Golgi to plasma membrane transport, exocytosis	NP_983592	<i>Eremothecium gossypii</i>	6e-14	83.6	51/128 (39%)
Asp2572	Weakly similar to yeast synaptobrevin (v-snare) homolog bos1	NP_593539	<i>Schizosaccharomyces pombe</i>	1e-30	135	77/214 (35%)
Asp2720	Similar to adapter-related protein complex 3 beta 1 subunit (Beta3A-adaptin)Adaptor protein complex AP-3 beta-1 subunit (AP-3complex beta-1 subunit) (Clathrin assembly protein complex 3 beta-1 large chain)	O00203	<i>Homo sapiens</i>	6e-34	150	88/191 (46%)
Asp2742	Secretory pathway ca2+-atpase	AAF37300	<i>Aspergillus niger</i>	1e-94	351	180/195 (92%)
Asp2795	myosin I myoA	A56511	<i>Aspergillus nidulans</i>	3e-18	98.2	51/60 (85%)
Asp2825	similar to ADP-ribosylation factor-like 2, contained ARF-like small GTPases domain	XP_394559	<i>Apis mellifera</i>	4e-27	121	54/79 (68%)
Asp2835	Similar to t snare complex subunit; syntaxin-like [schizosaccharomyces pombe]	NP_593832	<i>Schizosaccharomyces pombe</i>	1e-25	120	76/189 (40%)
Asp2898	Homologous to secretory pathway ca2+-atpase	AAF37300	<i>Aspergillus niger</i>	2e-36	158	78/79 (98%)
Asp2906	Similar to geranylgeranyl transferase type ii alpha subunit	O93829	<i>Candida albicans</i>	2e-39	166	89/210 (42%)

	(type ii protein geranyl-geranyltransferase alpha subunit) (GGTase-II-alpha) (PGGT) (YPT1/SEC4 proteins geranylgeranyltransferase alpha subunit)					
Asp2931	hypothetical protein AN6627.2 - SRP-dependent cotranslational membrane targeting, secretion related	EAA58156	<i>Aspergillus nidulans</i>	e-105	385	200/310 (64%)
Asp2935	Weakly similar to SEC14 cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PC TP).	P24280	<i>Saccharomyces cerevisiae</i>	8e-14	80.9	57/214 (26%)
Asp3240	Weakly similar to protein transport protein sec61-gamma subunit	NP_593061	<i>Schizosaccharomyces pombe</i>	1e-18	94.4	40/70 (57%)
Asp3374	<i>Aspergillus niger</i> srgb gene for a secretion related gtpase of the YPT/RAB family, exons 1-5	AJ278659	<i>Aspergillus niger</i>	0.0	252	123/123 (100%)
Asp3383	related to dock180 protein, involved in vesicle-mediated transport	CAE75725	<i>Neurospora crassa</i>	8e-67	260	129/240 (53%)
Asp3413	Similar to vacuolar protein sorting-associated protein vps35	O74552	<i>Schizosaccharomyces pombe</i>	1e-39	168	84/222 (37%)
Asp3534	Similar to protein that forms a heterotrimeric complex with erp2p, emp24p, and Erv25p; member, along with Emp24p and Erv25p, of the p24 family involved in ER to Golgi transport and localized to COPII-coated vesicles; Erp1p	NP_009402	<i>Saccharomyces cerevisiae</i>	9e-41	169	92/225 (40%)
Asp3633	Similar to protein transport protein sec73	O13817	<i>Schizosaccharomyces pombe</i>	8e-31	139	77/227 (33%)
Asp3645	Similar to gap1 protein	CAA22816	<i>Schizosaccharomyces pombe</i>	3e-19	100	52/93 (55%)
Asp3812	Vacuolar protein sorting-associated protein VPS13 (Intracellular trafficking and secretion)	Q07878	<i>Saccharomyces cerevisiae</i>	2e-29	136	77/221 (34%)
Asp3899	Similar to rab protein; involved in endocytosis	NP_594796	<i>Schizosaccharomyces pombe</i>	6e-38	160	72/125 (57%)
Asp3952	Vacuolar protein sorting-associated protein 74	Q06385	<i>Saccharomyces cerevisiae</i>	1e-23	114	49/136 (36%)
Asp4222	Similar to secretion related GTPase gtpase, (SrgA)	CAC17832	<i>Aspergillus niger</i>	3e-30	134	65/65 (100%)
Asp4247	Similar to related to secretion protein rsec8	XP_323530	<i>Neurospora crassa</i>	1e-41	176	89/171 (52%)
Asp4285	coatamer beta' subunit (beta' coat protein); secretory pathway	NP_596811	<i>Schizosaccharomyces pombe</i>	7e-39	166	73/111 (65%)
Asp4301	SED5-binding protein 2 (SEC24-related protein 2) Component of the COPII coat, that covers ER-derived vesicles involved in transport from the endoplasmic reticulum to the Golgi apparatus.	P53953	<i>Saccharomyces cerevisiae</i>	6e-29	133	78/183 (42%)

Asp4377	GTP-binding protein SARA (A.niger)	P52886	<i>Aspergillus niger</i>	1e-79	298	146/162 (90%)
Asp4401	Similar to endocytosis and cytoskeleton protein - Golgi to endosome transport, secretion related	NP_587759	<i>Schizosaccharomyces pombe</i>	9e-09	65.1	27/47 (57%)
Asp4442	Protein transport protein sec72	Q9P7V5	<i>Schizosaccharomyces pombe</i>	5e-41	174	92/224 (41%)
Asp4460	Coatomer beta subunit (Beta-coat protein) (Beta-COP)	Q9UUF7	<i>Schizosaccharomyces pombe</i>	4e-48	197	89/155 (57%)
Asp4991	Homologous to yeast component of copii coat of er-golgi vesicles, sec24	P40482	<i>Schizosaccharomyces pombe</i>	8e-59	232	115/236 (48%)
Asp5114	Secretion related GTPase gtpase, (SrgA)	CAC17832	<i>Aspergillus niger</i>	1e-64	248	122/122 (100%)
Asp5188	Similar to vesicular-fusion protein sec17 homolog	Q9P6A5	<i>Neurospora crassa</i>	7e-60	233	114/203 (56%)
Post-translational modification						
Asp170	Similar to alpha-1,2-mannosyltransferase; ktr3p	NP_009764	<i>Saccharomyces cerevisiae</i>	3e-24	116	63/130 (48%)
Asp370	Homologous to mannosyltransferase pmti - functional equivalence to Saccharomyces erevisiae PMT2	AAP05785	<i>Hypocrea jecorina</i>	5e-54	216	108/172 (62%)
Asp458	Weakly similar to 1,6-mannosyltransferase; involved in the outer chain elongation of N-linked oligosaccharides	NP_594852	<i>Schizosaccharomyces pombe</i>	8e-06	52.4	33/80 (41%)
Asp483	Similar to class i alpha-mannosidase 1a	AAG48160	<i>Aspergillus nidulans</i>	1e-46	192	104/239 (43%)
Asp521	mannosyl-oligosaccharide 1,2-alpha-mannosidase (ec 3.2.1.113) precursor	S63701	<i>Aspergillus phoenicis</i>	5e-98	361	178/184 (96%)
Asp1044	Weakly similar to alpha-1,3-mannosyltransferase	AAQ86764	<i>Cryptococcus neoformans</i>	1e-08	62.0	45/137 (32%)
Asp1109	Similar to mnn9p	AAK40024	<i>Pichia angusta</i>	6e-20	101	52/117 (44%)
Asp1117	Similar to dolichol phosphate mannose synthase- has been postulated to regulate the Trichoderma reesei secretory pathway.	BAB40714	<i>Aspergillus oryzae</i>	6e-51	203	100/106 (94%)
Asp1340	oligosaccharyltransferase alpha subunit	AAK08631	<i>Aspergillus niger</i>	3e-99	365	187/205 (91%)
Asp1344	Similar to mannosyl-oligosaccharide 1,2-alpha-mannosidase (Man(9)-alpha-mannosidase)	Q8J0Q0	<i>Candida albicans</i>	3e-55	219	107/214 (50%)
Asp1579	mannosyl-oligosaccharide 1,2-alpha-mannosidase (ec 3.2.1.113) precursor	S63701	<i>Aspergillus phoenicis</i>	3e-93	345	165/167 (98%)
Asp1594	Similar to class i alpha-mannosidase 1a	AAG48160	<i>Aspergillus nidulans</i>	e-137	493	275/534 (51%)
Asp1704	Weakly similar to alpha 1,6 mannosyltransferase	CAD91643	<i>Yarrowia lipolytica</i>	4e-12	73.6	48/161 (29%)
Asp2232	Similar to hypothetical protein AN9084.2, predicted	EAA61917	<i>Magnaporthe grisea</i>	3e-73	281	141/189 (74%)

	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity					
Asp2308	Homologous to udp-n-acetylglucosamine:dolichyl phosphate N-acetylglucosamine-1-phosphate transferase; GPT	AAL78196	<i>Aspergillus niger</i>	1e-20	104	52/70 (74%)
Asp2552	Homologous to glycosyl transferase, putative	CAF32096	<i>Aspergillus fumigatus</i>	4e-53	212	102/148 (68%)
Asp2774	sec53p - protein-ER targeting, secretion related phosphomannomutase	CAE52248	<i>Saccharomyces cerevisiae</i>	2e-36	154	70/87 (80%)
Asp3170	Weakly similar to mannosyltransferase	AAK54761	<i>Paracoccidioides brasiliensis</i>	1e-29	133	75/188 (39%)
Asp3205	Homologous to alpha-1, 2-mannosyltransferase [mips]	XP_326881	<i>Neurospora crassa</i>	5e-12	72.0	26/42 (61%)
Asp3381	Similar to alpha 1,6 mannosyltransferase	CAD91643	<i>Yarrowia lipolytica</i>	7e-67	257	119/209 (56%)
Asp3530	Weakly similar to possible mannosylphosphorylation protein mnn4 protein	CAF31981	<i>Aspergillus fumigatus</i>	5e-38	161	86/225 (38%)
Asp3936	dolichyl-phosphate beta-glucosyltransferase	T44819	<i>Ajellomyces capsulatus</i>	6e-80	301	145/169 (85%)
Asp4380	Similar to golgi mannosyltransferase complex subunit	CAE00652	<i>Kluyveromyces lactis</i>	8e-45	184	85/150 (56%)
Asp4472	Weakly similar to Pmt1p - transfers mannose residues from dolichyl phosphate-D-mannose to specific serine/threonine residues of proteins in the secretory pathway; acts in complex with Pmt2p	NP_010188	<i>Saccharomyces cerevisiae</i>	2e-25	121	56/176 (31%)
Asp4503	Similar to mannosyltransferase	NP_595123	<i>Schizosaccharomyces pombe</i>	2e-63	246	106/188 (56%)
Asp4598	Weakly similar to alpha 1,6 mannosyltransferase	CAD91643	<i>Yarrowia lipolytica</i>	1e-08	61.6	34/103 (33%)

^a- the function of genes were identified using GO annotation and BlastX to nr protein